

# SEQUENCE LISTING

<110> Monsanto Company

<120> TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROL  
COMPOUNDS AND TOCOPHEROLS

<130> MTC 6462.1

<140> 09/548,256

<141> 2000-04-12

<150> 60/128,995

<151> 1999-04-12

<160> 31

<170> PatentIn Ver. 2.1

<210> 1

<211> 43

<212> PRT

<213> jojoba

<400> 1

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Ile Tyr Ile Lys Thr Lys Lys Tyr Tyr Arg Ala  
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<210> 2

<211> 1258

<212> DNA

<213> Arabidopsis thaliana

<400> 2

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<210> 3

<211> 309

<212> PRT

<213> Arabidopsis thaliana

<400> 3

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 35 40 45

Leu Pro Val Thr Pro Gly Ser Lys Asp Lys Pro Val Val Leu Asn Ser  
 50 55 60

Lys Lys Ser Leu Lys Glu Tyr Cys Asp Gly Asn Asn Asn Ser Leu Thr  
 65 70 75 80

Val Val Phe Lys Asp Leu Gly Ala Gln Val Ser Tyr Arg Thr Leu Phe  
 85 90 95

Phe Phe Glu Tyr Leu Gly Pro Leu Leu Ile Tyr Pro Val Phe Tyr Tyr  
 100 105 110

Phe Pro Val Tyr Lys Phe Leu Gly Tyr Gly Glu Asp Cys Val Ile His  
 115 120 125

Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys  
 130 135 140

Arg Ile Leu Glu Thr Phe Phe Val His Arg Phe Ser His Thr Ser Pro  
 145 150 155 160

Ile Gly Asn Val Phe Arg Asn Cys Ala Tyr Tyr Trp Ser Phe Gly Ala  
 165 170 175

Tyr Ile Ala Tyr Tyr Val Asn His Pro Leu Tyr Thr Pro Val Ser Asp  
 180 185 190

Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Leu Val Cys Gln Val Ala  
 195 200 205

Asn Phe Tyr Cys His Ile Leu Leu Lys Asn Leu Arg Asp Pro Ser Gly  
 210 215 220

Ala Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val Thr  
 225 230 235 240

Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Leu Gly Phe Asn Ile  
 245 250 255

Ala Thr Gln Thr Ile Ala Gly Tyr Val Phe Leu Ala Val Ala Ala Leu  
 260 265 270

Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Arg Lys Ile  
 275 280 285

Phe Asp Gly Lys Asp Gly Lys Pro Lys Tyr Pro Arg Arg Trp Val Ile  
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Leu Pro Pro Phe Leu  
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<211> 1361

<212> DNA

<213> Zea mays

<400> 4

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<210> 5

<211> 309

<212> PRT

<213> Zea mays

<400> 5

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Met Lys Val Thr Val Val Ser Arg Ser Gly Arg Glu Val Val Lys Gly
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Gly Ile Asp Leu Lys Asp Ser Ala Lys Val Ala Asp Leu Gln Glu Ala
      20             25             30

```

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Ile His Ala Arg Thr Lys Lys Tyr Tyr Pro Ser Arg Gln Arg Leu Thr
      35             40             45

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Leu Pro Leu Gln Pro Gly Lys Gly Gly Lys Pro Val Val Leu Ser Pro
      50             55             60

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Lys Ala Ser Leu Leu Glu Tyr Cys Glu Lys Gly Ser Gly Ser Leu Thr
      65             70             75             80

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Val Val Phe Lys Asp Leu Gly Pro Gln Val Tyr Tyr Ser Thr Leu Phe
      85             90             95

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Phe Phe Glu Tyr Leu Gly Pro Leu Ile Ile Tyr Pro Met Phe Tyr Tyr
      100            105            110

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Leu Pro Val Tyr Lys Tyr Phe Gly His Glu Gly Glu Arg Ala Met His
      115            120            125

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Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys  
 130 135 140  
 Arg Ile Met Glu Thr Phe Phe Val His Arg Phe Ser Ala Thr Ser Pro  
 145 150 155 160  
 Leu Ser Asn Val Phe Arg Asn Cys Ala Tyr Tyr Trp Thr Phe Gly Ala  
 165 170 175  
 Tyr Ile Ala Tyr Tyr Cys Asn His Pro Leu Tyr Thr Pro Val Ser Asp  
 180 185 190  
 Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Val Val Cys Gln Val Ala  
 195 200 205  
 Asn Phe Tyr Cys His Ile Leu Leu Arg Asn Leu Arg Ser Pro Ser Gly  
 210 215 220  
 Ser Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val Thr  
 225 230 235 240  
 Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Val Gly Phe Asn Ile  
 245 250 255  
 Ala Thr Gln Thr Val Ala Gly Tyr Val Phe Leu Val Val Ala Ala Gly  
 260 265 270  
 Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Lys Lys Leu  
 275 280 285  
 Phe Asp Gly Lys Asp Gly Arg Pro Lys Tyr Pro Arg Arg Trp Val Ile  
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 Leu Pro Pro Phe Leu  
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<210> 6

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<212> DNA

<213> Glycine max

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<210> 7

<211> 244

<212> PRT

<213> Glycine max

<400> 7

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Met Ser Val Ile Ser Leu Val Ser Leu Ala Asn Ala Gly Phe Ser Glu
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Ile Arg Gly Lys His Leu Asn Tyr Ser Lys Phe Trp Asn Ala Asn Pro
      20             25            30

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```

Ser Ala Glu Lys Gln Val Lys Leu Ser Ser Lys Ala Gly Met Leu Leu
      35             40            45

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```

Leu Tyr Thr Pro Ala Phe Leu Ala Gly Leu Ala Ser Phe Trp Ile Phe
      50             55            60

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```

Pro His Gln Gly Leu Arg Ser Thr Leu Leu Gln Ser Ala Val Thr Leu
      65             70            75            80

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His Phe Phe Lys Arg Val Phe Glu Val Val Phe Ile His Lys Tyr Ser
      85             90            95

```

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Gly Ala Met Leu Leu Asp Ser Ala Ile Pro Ile Thr Leu Ser Tyr Phe
      100            105            110

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```

Leu Ser Thr Ala Thr Met Ile Tyr Ala Gln His Leu Thr Gln Gly Leu
      115            120            125

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Pro Glu Pro Pro Ile Asp Leu Leu Tyr Pro Gly Ile Val Leu Phe Val
      130            135            140

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Val Gly Ile Ile Gly Asn Phe Tyr His His Tyr Leu Leu Ser Asn Leu
      145            150            155            160

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Arg Gly Lys Gly Glu Lys Glu Tyr Lys Ile Pro Lys Gly Gly Met Phe  
165 170 175

Glu Leu Val Ile Cys Pro His Tyr Leu Phe Glu Ile Ile Glu Phe Tyr  
180 185 190

Gly Phe Ser Phe Ile Ser Gln Thr Leu Tyr Ala Phe Ser Phe Thr Val  
195 200 205

Gly Thr Thr Leu Tyr Leu Leu Gly Arg Ser Tyr Ser Thr Arg Lys Trp  
210 215 220

Tyr Leu Ser Lys Phe Glu Asp Phe Pro Glu His Val Lys Ala Ile Ile  
225 230 235 240

Pro Phe Val Phe

<210> 8  
<211> 917  
<212> DNA  
<213> Glycine max

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<210> 9  
<211> 266  
<212> PRT  
<213> Glycine max

<400> 9

Met Val Ile Lys Ser Val Leu Phe Ser Phe Ile Phe Pro Pro Pro Pro  
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Asn Ala Phe Leu Ser Glu Ile Arg Gly Lys His Leu Asn Tyr Ser Lys  
35 40 45

Phe Trp Asn Ala Asn Pro Ser Ala Glu Lys Gln Val Lys Leu Ser Ser  
50 55 60

Lys Ala Gly Met Leu Leu Leu Tyr Thr Pro Ala Phe Leu Ala Gly Leu  
65 70 75 80

Ala Ser Phe Trp Val Phe Pro His Gln Gly Leu Arg Phe Thr Ile Leu  
85 90 95

Gln Ser Ala Val Thr Leu His Tyr Phe Lys Arg Val Phe Glu Gly Leu  
100 105 110

Phe Ile His Lys Tyr Ser Gly Gly Met Thr Leu Glu Ser Ala Ile Pro  
115 120 125

Ile Thr Leu Ser Tyr Phe Leu Ser Ala Val Thr Met Val Tyr Ser Gln  
130 135 140

His Leu Thr Lys Gly Phe Pro Glu Pro Pro Ile Asn Leu Phe Tyr Pro  
145 150 155 160

Gly Ile Val Leu Phe Leu Val Gly Ile Ile Gly Asn Phe Tyr His His  
165 170 175

Tyr Leu Leu Ser Lys Leu Arg Gly Lys Gly Glu Lys Glu Tyr Lys Ile  
180 185 190

Pro Lys Gly Gly Phe Phe Glu Leu Val Ile Cys Pro His Tyr Phe Phe  
195 200 205

Glu Ile Thr Val Phe Tyr Gly Ile Phe Phe Ile Ser Gln Thr Leu Tyr  
210 215 220

Ser Phe Ala Phe Ala Val Gly Thr Thr Met Tyr Leu Val Gly Arg Ser  
225 230 235 240

Tyr Ser Thr Arg Lys Trp Tyr Leu Ser Lys Phe Glu Asp Phe Pro Lys



His Val Lys Ala Val Ile Pro Phe Val Phe

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265

<210> 10

<211> 1942

<212> DNA

<213> *Arabidopsis thaliana*

<400> 10

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<210> 11

<211> 520  
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 <213> Arabidopsis thaliana

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Ser Asp Ser Ser Asn Gly Leu Leu Leu Ser Gly Ser Asp Asn Asn Ser  
 35 40 45

Pro Ser Asp Asp Val Gly Ala Pro Ala Asp Val Arg Asp Arg Ile Asp  
 50 55 60

Ser Val Val Asn Asp Asp Ala Gln Gly Thr Ala Asn Leu Ala Gly Asp  
 65 70 75 80

Asn Asn Gly Gly Gly Asp Asn Asn Gly Gly Gly Arg Gly Gly Gly Glu  
 85 90 95

Gly Arg Gly Asn Ala Asp Ala Thr Phe Thr Tyr Arg Pro Ser Val Pro  
 100 105 110

Ala His Arg Arg Ala Arg Glu Ser Pro Leu Ser Ser Asp Ala Ile Phe  
 115 120 125

Lys Gln Ser His Ala Gly Leu Phe Asn Leu Cys Val Val Val Leu Ile  
 130 135 140

Ala Val Asn Ser Arg Leu Ile Ile Glu Asn Leu Met Lys Tyr Gly Trp  
 145 150 155 160

Leu Ile Arg Thr Asp Phe Trp Phe Ser Ser Arg Ser Leu Arg Asp Trp  
 165 170 175

Pro Leu Phe Met Cys Cys Ile Ser Leu Ser Ile Phe Pro Leu Ala Ala  
 180 185 190

Phe Thr Val Glu Lys Leu Val Leu Gln Lys Tyr Ile Ser Glu Pro Val  
 195 200 205

Val Ile Phe Leu His Ile Ile Ile Thr Met Thr Glu Val Leu Tyr Pro  
 210 215 220

Val Tyr Val Thr Leu Arg Cys Asp Ser Ala Phe Leu Ser Gly Val Thr

225		230		235		240
Leu Met Leu Leu Thr Cys Ile Val Trp Leu Lys Leu Val Ser Tyr Ala						
	245		250		255	
His Thr Ser Tyr Asp Ile Arg Ser Leu Ala Asn Ala Ala Asp Lys Ala						
	260		265		270	
Asn Pro Glu Val Ser Tyr Tyr Val Ser Leu Lys Ser Leu Ala Tyr Phe						
	275		280		285	
Met Val Ala Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg Ser Ala						
	290		295		300	
Cys Ile Arg Lys Gly Trp Val Ala Arg Gln Phe Ala Lys Leu Val Ile						
305		310		315		320
Phe Thr Gly Phe Met Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro Ile						
	325		330		335	
Val Arg Asn Ser Lys His Pro Leu Lys Gly Asp Leu Leu Tyr Ala Ile						
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Glu Arg Val Leu Lys Leu Ser Val Pro Asn Leu Tyr Val Trp Leu Cys						
	355		360		365	
Met Phe Tyr Cys Phe Phe His Leu Trp Leu Asn Ile Leu Ala Glu Leu						
	370		375		380	
Leu Cys Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys						
385		390		395		400
Ser Val Gly Asp Tyr Trp Arg Met Trp Asn Met Pro Val His Lys Trp						
	405		410		415	
Met Val Arg His Ile Tyr Phe Pro Cys Leu Arg Ser Lys Ile Pro Lys						
	420		425		430	
Thr Leu Ala Ile Ile Ile Ala Phe Leu Val Ser Ala Val Phe His Glu						
	435		440		445	
Leu Cys Ile Ala Val Pro Cys Arg Leu Phe Lys Leu Trp Ala Phe Leu						
	450		455		460	
Gly Ile Met Phe Gln Val Pro Leu Val Phe Ile Thr Asn Tyr Leu Gln						
465		470		475		480
Glu Arg Phe Gly Ser Thr Val Gly Asn Met Ile Phe Trp Phe Ile Phe						

Cys Ile Phe Gly Gln Pro Met Cys Val Leu Leu Tyr Tyr His Asp Leu  
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Met Asn Arg Lys Gly Ser Met Ser  
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<210> 12

<211> 381

<212> DNA

<213> *Caenorhabditis elegans*

<220>

<221> unsure

<222> (46)

<223> n=a,t,c or g

<400> 12

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<210> 13

<211> 300

<212> DNA

<213> *Caenorhabditis elegans*

<400> 13

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cgacctgtaa tacatgaaaa atatcaatag gaattttgag ataatttggc aacatgcaat 180
ataatgatta taataaaaaaa cttgtcttaa gactagagaa ctgctaattc aaaaaaaca 240
aattgagata aatcaaatac caacggtttg gttttgaact gctgaaacac caaagttcaa 300
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<210> 14

<211> 496

<212> PRT

<213> *Caenorhabditis elegans*

<400> 14

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Asn	Gly	Ser	Leu	Ala	Ser	Ser	Arg	Arg	Ser	Ser	Phe	Ala	Gln	Asn	Gly	20	25	30	
Asn	Ser	Ser	Arg	Lys	Ser	Ser	Glu	Met	Arg	Gly	Pro	Cys	Glu	Lys	Val	35	40	45	
Val	His	Thr	Ala	Gln	Asp	Ser	Leu	Phe	Ser	Thr	Ser	Ser	Gly	Trp	Thr	50	55	60	
Asn	Phe	Arg	Gly	Phe	Phe	Asn	Leu	Ser	Ile	Leu	Leu	Leu	Val	Leu	Ser	65	70	75	80
Asn	Gly	Arg	Val	Ala	Leu	Glu	Asn	Val	Ile	Lys	Tyr	Gly	Ile	Leu	Ile	85	90	95	
Thr	Pro	Leu	Gln	Trp	Ile	Ser	Thr	Phe	Val	Glu	His	His	Tyr	Ser	Ile	100	105	110	
Trp	Ser	Trp	Pro	Asn	Leu	Ala	Leu	Ile	Leu	Cys	Ser	Asn	Ile	Gln	Ile	115	120	125	
Leu	Ser	Val	Phe	Gly	Met	Glu	Lys	Ile	Leu	Glu	Arg	Gly	Trp	Leu	Gly	130	135	140	
Asn	Gly	Phe	Ala	Ala	Val	Phe	Tyr	Thr	Ser	Leu	Val	Ile	Ala	His	Leu	145	150	155	160
Thr	Ile	Pro	Val	Val	Val	Thr	Leu	Thr	His	Lys	Trp	Lys	Asn	Pro	Leu	165	170	175	
Trp	Ser	Val	Val	Met	Met	Gly	Val	Tyr	Val	Ile	Glu	Ala	Leu	Lys	Phe	180	185	190	
Ile	Ser	Tyr	Gly	His	Val	Asn	Tyr	Trp	Ala	Arg	Asp	Ala	Arg	Arg	Lys	195	200	205	
Ile	Thr	Glu	Leu	Lys	Thr	Gln	Val	Thr	Asp	Leu	Ala	Lys	Lys	Thr	Cys	210	215	220	
Asp	Pro	Lys	Gln	Phe	Trp	Asp	Leu	Lys	Asp	Glu	Leu	Ser	Met	His	Gln	225	230	235	240
Met	Ala	Ala	Gln	Tyr	Pro	Ala	Asn	Leu	Thr	Leu	Ser	Asn	Ile	Tyr	Tyr	245	250	255	

Phe Met Ala Ala Pro Thr Leu Cys Tyr Glu Phe Lys Phe Pro Arg Leu  
260 265 270

Leu Arg Ile Arg Lys His Phe Leu Ile Lys Arg Thr Val Glu Leu Ile  
275 280 285

Phe Leu Ser Phe Leu Ile Ala Ala Leu Val Gln Gln Trp Val Val Pro  
290 295 300

Thr Val Arg Asn Ser Met Lys Pro Leu Ser Glu Met Glu Tyr Ser Arg  
305 310 315 320

Cys Leu Glu Arg Leu Leu Lys Leu Ala Ile Pro Asn His Leu Ile Trp  
325 330 335

Leu Leu Phe Phe Tyr Thr Phe Phe His Ser Phe Leu Asn Leu Ile Ala  
340 345 350

Glu Leu Leu Arg Phe Ala Asp Arg Glu Phe Tyr Arg Asp Phe Trp Asn  
355 360 365

Ala Glu Thr Ile Gly Tyr Phe Trp Lys Ser Trp Asn Ile Pro Val His  
370 375 380

Arg Phe Ala Val Arg His Ile Tyr Ser Pro Met Met Arg Asn Asn Phe  
385 390 395 400

Ser Lys Met Ser Ala Phe Phe Val Val Phe Phe Val Ser Ala Phe Phe  
405 410 415

His Glu Tyr Leu Val Ser Val Pro Leu Lys Ile Phe Arg Leu Trp Ser  
420 425 430

Tyr Tyr Gly Met Met Gly Gln Ile Pro Leu Ser Ile Ile Thr Asp Lys  
435 440 445

Val Val Arg Gly Gly Arg Thr Gly Asn Ile Ile Val Trp Leu Ser Leu  
450 455 460

Ile Val Gly Gln Pro Leu Ala Ile Leu Met Tyr Gly His Asp Trp Tyr  
465 470 475 480

Ile Leu Asn Phe Gly Val Ser Ala Val Gln Asn Gln Thr Val Gly Ile  
485 490 495

<210> 15  
<211> 257  
<212> DNA  
<213> Glycine max

<400> 15  
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ggcttttggg aaaactggca tgcttccttc aacaagtggc ttgtgaggta tatatacatt 120  
cctcttgggg gatctaagaa aaagctacta aatgtgtggg ttgttttcac atttgttgca 180  
atctggcatg atttagagtg gaagcttctt tcatgggcat gggtgacgtg tttattcttc 240  
atccctgagt tggtttt 257

<210> 16  
<211> 234  
<212> DNA  
<213> Glycine max

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<220>  
<221> unsure  
<222> (41)  
<223> n=a, t, c or g

<220>  
<221> unsure  
<222> (60)  
<223> n=a, t, c or g

<400> 16  
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ctatcctcgc acaccttata ttcgaaaggg ttggctgttt cgccaacttg tcaactgata 120  
atatttacag gagttatggg atttataata gaacaatata ttaatcccat tgtacaaaat 180  
tcacagcatc ctctcaaggg aaaccttctt tacgccatcg agagagttct gaag 234

<210> 17  
<211> 275  
<212> DNA  
<213> Glycine max

<220>  
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<222> (192)  
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 <222> (202)  
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 <222> (204)  
 <223> n=a, t, c or g  
  
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 <222> (211)  
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 <222> (222)  
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 <222> (234)  
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 <222> (238) .. (239)  
 <223> n=a, t, c or g  
  
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 <221> unsure  
 <222> (244) .. (245)  
 <223> n=a, t, c or g  
  
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 <221> unsure  
 <222> (251)  
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 <220>  
 <221> unsure  
 <222> (262) .. (263)  
 <223> n=a, t, c or g



<400> 17

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gatgatccgc cacctatatt ttccatgttt aaggcacggg ataccaaagg ccgttgctct 120
tttaattgcc ttectgggtc tgetttatcc catgagctgt gcatcgctgt tccttgccca 180
catattcaag tngtgggttt cngnggaatt nagtttcagg tnccttgggt ttcnaccnna 240
attntnnggc naaaaaattc cnngaacccc gggggg 275
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<210> 18

<211> 267

<212> DNA

<213> Glycine max

<400> 18

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ctgcttttgt atctgggtgc acgttgatgc tattaacttg cattgtgtgg ttaaaattgg 60
tgtcatatgc acatacaaac tatgatatga gagcacttac tgtttcgaat gaaaagggag 120
aaacattacc caatactttg atatggagta tccgtacact gtgaccttca ggagtttggc 180
atacttcatg gttgctccta cattatgcta tcagacaagc tatectcgca cacettcagt 240
tcgaaagggg tgggtgtttc gtcaact 267
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<210> 19

<211> 1895

<212> DNA

<213> Human

<220>

<221> unsure

<222> (209)

<223> n=a, t, c or g

<400> 19

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tgggtgctga gtctcagagc ttggcatgga gaccagacag ggctgggtct gcaagcctga 120
ggctgccgcc ctgagctcgg gctgggacgt gccagaggt gttgggagga tctgggggtga 180
gtacctgtg gccaggacta aaggggctnc accctcctgt ccatecctcg cagatcttga 240
gcaatgcccg gttatttctg gagaacctca tcaagtatgg catcctgggtg gaccccatcc 300
aggtggtttc tctgttcctg aaggatccct atagctgggc cgcccatgc ctggttattg 360
cggccaatgt ctttgtctg gctgcattcc aggttgagaa gcgcctggcg gtgggtgccc 420
tgacggagca ggcgggactg ctgctgcacg tggccaacct ggccaccatt ctgtgtttcc 480
cagcggctgt ggtcttactg gttgagtcta tcaactcagt gggctccctg ctggcgctga 540
tggcgcacac catcctcttc ctcaagctct tctcctaccg cgacgtcaac tcatggtgcc 600
gcagggccag ggccaaggct gcctctgcag ggaagaaggc cagcagtgtc gctgccccgc 660
acaccgtgag ctaccoggac aatctgacct acccgatct ctactacttc ctcttcgccc 720
ccacctgtg ctacgagtc aactttcccc gctctccccg catccggaag cgctttctgc 780
tgcgacggat ccttgagatg ctgttcttca ccagctcca ggtggggctg atccagcagt 840
ggatggtccc caccatccag aactccatga agcccttcaa ggacatggac tactcacgca 900
tcacgagcg ctcctgaag ctggcggtcc ccaatcacct catctggctc atcttcttct 960
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actggctctt ccactcctgc ctgaatgccg tggctgagct catgcagttt ggagaccggg 1020
agttctaccg ggactggtgg aactccgagt ctgtcaccta cttctggcag aactggaaca 1080
tcctgtgca caagtgggtgc atcagacact tctacaagcc catgcttcga cggggcagca 1140
gcaagtggat ggccaggaca ggggtgttcc tggcctcggc cttcttccac gagtacctgg 1200
tgagcgtccc tctgcgaatg ttccgcctct gggcggtcac gggcatgatg gctcagatcc 1260
cactggcctg gttcgtgggc cgctttttcc agggcaacta tggcaacgca gctgtgtggc 1320
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tcaactatga ggccccagcg gcagaggcct gagctgcacc tgagggcctg gcttctcact 1440
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ctgtcctgca cccctcaggg atggcgacag caggccagac acagtctgat gccagctggg 1620
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gggcgggcat ggccggtagg gggagtgcaa ggccaggcag acgcccccat tccccacact 1860
cccctaccta gaaaagctca gctcaggcgt cctct 1895

```

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<210> 20
<211> 519
<212> DNA
<213> Montierella alphina

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<223> n=a, t, c or g

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<220>
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<223> n=a, t, c or g

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<220>
<221> unsure
<222> (48)
<223> n=a, t, c or g

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<220>
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<222> (52)
<223> n=a, t, c or g

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<220>  
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<222> (102)..(103)  
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<222> (113)  
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<220>  
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<222> (148)

<223> n=a, t, c or g

<220>

<221> unsure

<222> (430)

<223> n=a, t, c or g

<400> 20

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ttanactnaa ttngaaaatn cnnncccaac tttaggnact tnnagncccc ccnacttgac 120
aacggagcac tatatttacc ccgtggtngt tcaaccacgc catctcacc ttgcgagcat 180
tggtgctgct cttgataccc ttcagtctta actatctcat gatcttttac atcattttcg 240
agtgcacctg caacgccttt gcggaactaa gttgctttgc ggatcgcaac ttttacgagg 300
attggtggaa ctgcgtcagc tttgatgagt gggcacgcaa atggaacaag cctgtgcaac 360
acttcttgct ccgccacgtg tacgactcga gcacccgagt ccttccactt gtccgaaatc 420
caatgccgcn aattgcaaac gttccttccc ggtcgtcaat gcgttcaacg aacctgggtg 480
aagaatgggt ggtgacaacg ttaaagtgcg cccggtatc 519
```

<210> 21

<211> 518

<212> DNA

<213> mouse

<400> 21

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tggaggacaa cgcgggggtct gatacgactc actatagggg atttggccct cgagcagtag 60
attcggcacg atgggcacga ggactccatc atgttcctca agctttattc ctaccgggat 120
gtcaacctgt ggtgccgcca gcgaagggtc aaggccaaag ctgtctctac aggaagaag 180
gtcagtgggg ctgctgcgag caagctgtga gctatccaga caacctgacc taccgagatc 240
tcgattactt catctttgct cctactttgt gttatgaact caactttcct cgggtccccc 300
gaatacgaga gcgctttctg ctacgacgag ttcttgagat gctctttttt acccagcttc 360
aagtggggct gatccaacag tggatggtcc ctactatcca gaactccatg gaagcccttt 420
caagagcttc tgcagttttg gagaccgca gttctacaga gattggtgga atgctgagtc 480
tgtcaccgac ttttggcaga actggaatat ccccggtg 518
```

<210> 22

<211> 299

<212> DNA

<213> mouse

<400> 22

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ccatgatggc tcaggtccca ctggcctgga ttgtgggccc attcttccaa gggaactatg 60
gcaatgcagc tgtgtgggtg acactcatca ttgggcaacc ggtggctgtc tcatgtatgt 120
ccacgactac tacgtgctca actacgatgc cccagtgggt catgagctac tgccaaaggc 180
agccctccct aacctgggccc tggagtcttg gaggggttcc tggctgcctg cacactcctc 240
ctagtctggg aggcctctct gccctatgc gctactcctg ctcttgggga tggcatttg 299
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<210> 23  
 <211> 1766  
 <212> DNA  
 <213> Rat

<400> 23  
 cacgactggg ccgcgacgtg gtgcggggccg aagccatggg cgaccgcgga ggcgcgggaa 60  
 gctctcggcg tcggaggacc ggctcgcggg ttcccatcca gggtagtagt gggcccatgg 120  
 tagacgaaga ggaggtgcga gacgccgctg tgggccccga cttgggcgcc gggggtgacg 180  
 ctccggctcc ggctccggtt ccggctccag cccacaccgc ggacaaagac cggcagacca 240  
 gcgtgggcga cggccactgg gagctgaggt gccatcgtct gcaagactct ttgttcagct 300  
 cagacagcgg tttcagcaat taccgtggta tcctgaattg gtgcgtgggt atgctgatcc 360  
 tgagtaatgc aaggttattt ttagagaatc ttatcaagta tggcatcctg gtggatccca 420  
 tccagggtgt gtctctgttt ctgaaggacc cctacagctg gcctgccccca tgettgatca 480  
 ttgcatccaa tatctttatt gtggctacat ttcagattga gaagcgctg tcagtgggtg 540  
 ccctgacaga gcagatgggg ctgctgctac atgtgggttaa cctggccaca attatctgct 600  
 tcccagcagc tgtggcctta ctggttgagt ctatcactcc agtgggttcc ctgtttgctc 660  
 tggcatcata ctccatcatc ttctcaagc ttttctccta ccgggatgtc aatctgtggt 720  
 gccgccagcg aaggggtcaag gccaaaagctg tgtctgcagg gaagaaggtc agtggggctg 780  
 ctgcccagaa cactgtaagc tatccggaca acctgacctc ccgagatctc tattacttca 840  
 tctttgctcc tactttgtgt tatgaactca actttcctcg atcccccca atacgaaagc 900  
 gctttctgct acggcggggt cttgagatgc tctttttcac ccagcttcaa gtggggctga 960  
 tccagcagtg gatggctcct actatccaga actccatgaa gcccttcaag gacatggact 1020  
 attcacgaat cattgagcgt ctcttaaagc tggcgggtccc caaccatctg atatggctca 1080  
 tcttcttcta ttggcttttc cactcatgtc tcaatgctgt ggcagagctc ctgcagtttg 1140  
 gagaccgcga gttctacagg gactgggtgga atgctgagtc tgtcacctac ttttggcaga 1200  
 actggaatat ccccggtgcac aagtgggtgca tcagacactt ctacaagcct atgctcagac 1260  
 tgggcagcaa caaatggatg gccaggactg gggctttttt ggcgtcagcc ttcttccatg 1320  
 agtacctagt gagcattccc ctgaggatgt tccgcctctg ggcattcaca gccatgatgg 1380  
 ctcagggtccc actggcctgg attgtgaacc gcttcttcca agggaaactat ggcaatgcag 1440  
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 actacgtgct caactatgat gcccagtggt gggcctgagc tactgccaaa ggccagccct 1560  
 ccctaacctg ggcttgaggt tctggagggc ttcttggtgt cctgcacact cctcctagtc 1620  
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 agctatctaa aaaaaaaaaa aaaaaa 1766

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 <211> 500  
 <212> PRT  
 <213> rat

<400> 24  
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Glu	Val	Arg	Asp	Ala	Ala	Val	Gly	Pro	Asp	Leu	Gly	Ala	Gly	Gly	Asp			
		35					40					45						
Ala	Pro	Ala	Pro	Ala	Pro	Val	Pro	Ala	Pro	Ala	His	Thr	Arg	Asp	Lys			
		50				55					60							
Asp	Arg	Gln	Thr	Ser	Val	Gly	Asp	Gly	His	Trp	Glu	Leu	Arg	Cys	His			
	65				70					75					80			
Arg	Leu	Gln	Asp	Ser	Leu	Phe	Ser	Ser	Asp	Ser	Gly	Phe	Ser	Asn	Tyr			
				85					90					95				
Arg	Gly	Ile	Leu	Asn	Trp	Cys	Val	Val	Met	Leu	Ile	Leu	Ser	Asn	Ala			
			100					105					110					
Arg	Leu	Phe	Leu	Glu	Asn	Leu	Ile	Lys	Tyr	Gly	Ile	Leu	Val	Asp	Pro			
		115				120						125						
Ile	Gln	Val	Val	Ser	Leu	Phe	Leu	Lys	Asp	Pro	Tyr	Ser	Trp	Pro	Ala			
	130					135						140						
Pro	Cys	Leu	Ile	Ile	Ala	Ser	Asn	Ile	Phe	Ile	Val	Ala	Thr	Phe	Gln			
145					150				155						160			
Ile	Glu	Lys	Arg	Leu	Ser	Val	Gly	Ala	Leu	Thr	Glu	Gln	Met	Gly	Leu			
				165					170					175				
Leu	Leu	His	Val	Val	Asn	Leu	Ala	Thr	Ile	Ile	Cys	Phe	Pro	Ala	Ala			
		180						185					190					
Val	Ala	Leu	Leu	Val	Glu	Ser	Ile	Thr	Pro	Val	Gly	Ser	Leu	Phe	Ala			
		195					200					205						
Leu	Ala	Ser	Tyr	Ser	Ile	Ile	Phe	Leu	Lys	Leu	Phe	Ser	Tyr	Arg	Asp			
	210					215					220							
Val	Asn	Leu	Trp	Cys	Arg	Gln	Arg	Arg	Val	Lys	Ala	Lys	Ala	Val	Ser			
225					230					235					240			
Ala	Gly	Lys	Lys	Val	Ser	Gly	Ala	Ala	Ala	Gln	Asn	Thr	Val	Ser	Tyr			
				245					250					255				
Pro	Asp	Asn	Leu	Thr	Tyr	Arg	Asp	Leu	Tyr	Tyr	Phe	Ile	Phe	Ala	Pro			
			260					265					270					

Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys  
 275 280 285

Arg Phe Leu Leu Arg Arg Val Leu Glu Met Leu Phe Phe Thr Gln Leu  
 290 295 300

Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile Gln Asn Ser  
 305 310 315 320

Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu  
 325 330 335

Leu Lys Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr  
 340 345 350

Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Leu Gln Phe  
 355 360 365

Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ala Glu Ser Val Thr  
 370 375 380

Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg  
 385 390 395 400

His Phe Tyr Lys Pro Met Leu Arg Leu Gly Ser Asn Lys Trp Met Ala  
 405 410 415

Arg Thr Gly Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val  
 420 425 430

Ser Ile Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Ala Met Met  
 435 440 445

Ala Gln Val Pro Leu Ala Trp Ile Val Asn Arg Phe Phe Gln Gly Asn  
 450 455 460

Tyr Gly Asn Ala Ala Val Trp Val Thr Leu Ile Ile Gly Gln Pro Val  
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Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Asp Ala  
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Pro Val Gly Ala  
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<222> (317)

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aagatatctc catgctacgt tcaagcatgt aatgggtggc aacatgatan tttggntctn 180
cagtatagtc ggacagccga tgtnnnnna tctatactac catgacgtca tgaacaggca 240
ggcccaggca agtagatagt ncggcagaga catgtacttc aacatcganc atcagnagca 300
nacngagcga gcggcangaa ncagc 325
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<210> 26

<211> 262

<212> DNA

<213> Zea mays

<400> 26

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aaagttggca ttcaacaatc tcattagtgga tcctgctact acctgttttc acatcctttt 180
tacaacattt gaaattgtat atccagtgcg cgtgattctt aagtgtgatt ctgcagtttt 240
acaggccttg tgttgatggt ta 262
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 <211> 253  
 <212> DNA  
 <213> Zea mays

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 atgagttatg tgttgctgtt ccctgccaca tactcaagtt ctgggctttt ttttaggaatc 180  
 atgcttcaga ttccccctcat catattgaca tcatacctca aaaataaatt cagtgcacaca 240  
 atgggttgga ata 253

<210> 28  
 <211> 254  
 <212> DNA  
 <213> Zea mays

<400> 28  
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 aaaagtggc attcaacaat ctcatatgtg atcctgctac tacctgtttt cacatccttt 180  
 ttacaacatt tgaaattgta tatccagtgc tcgtgattct taagtgtgat tctgcagttt 240  
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 <213> Maize

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 ggacaactgc aagccctgcg gcggcgctat cccgctgtgc atggtgtcgg agttcgacct 180  
 gccgctcgac ctctgtggacc gcaaggtgag gaagatgaag atgatttcgc cgtccaacgt 240  
 cgccgctcgac atcggccgca cgctcgcgcc ccacgagtac atcgggatgg tcaggcgca 300  
 ggtgctcgac gcctacctcc gctcacgggc acagtccgtc ggcgcgagg tcgtcaacgg 360  
 cctcttcta aggtacgagg cgcccaaaga gccgaacggc tcgtacgtgg tgcactacaa 420  
 ccactacgac ggagcaacg gcaaggtcgg cggcgagaag cggtcgttcg aggtggacgc 480  
 gatcgtgggc gcggacggcg ccaactctcg cgtggccaac gacatgggag cgggcgacta 540  
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 cgaggagcgc gcggagatgt acgtcggcga cgacgtctct cccgacttct acggctgggt 660  
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gcggagagga agagaaacaa gttgtgcaag tgcagcaagt agatcaaaag tgctgcctgt 1440
ttgtatcgat ggatcctgca acatatagca tctgggtgat ttgagaattc ggagcagttc 1500
atcgactgga ttctgacgcc ggcaagcatc gacgtcaatg aatgtctaata acttagtaca 1560
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<211> 541

<212> PRT

<213> Maize

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<221> UNSURE

<222> (520)

<223> Xaa=any amino acid

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20 25 30

Met Asp Asn Cys Lys Pro Cys Gly Gly Ala Ile Pro Leu Cys Met Val  
35 40 45

Ser Glu Phe Asp Leu Pro Leu Asp Leu Val Asp Arg Lys Val Arg Lys  
50 55 60

Met Lys Met Ile Ser Pro Ser Asn Val Ala Val Asp Ile Gly Arg Thr  
65 70 75 80

Leu Ala Pro His Glu Tyr Ile Gly Met Val Arg Arg Glu Val Leu Asp  
85 90 95

Ala Tyr Leu Arg Ser Arg Ala Gln Ser Val Gly Ala Glu Val Val Asn  
100 105 110

Gly Leu Phe Leu Arg Tyr Glu Ala Pro Lys Glu Pro Asn Gly Ser Tyr  
115 120 125

Val Val His Tyr Asn His Tyr Asp Gly Ser Asn Gly Lys Val Gly Gly  
130 135 140

Glu Lys Arg Ser Phe Glu Val Asp Ala Ile Val Gly Ala Asp Gly Ala  
145 150 155 160

Asn Ser Arg Val Ala Asn Asp Met Gly Ala Gly Asp Tyr Glu Tyr Ala  
165 170 175

Ile Ala Phe Gln Glu Arg Val Lys Ile Pro Asp Asp Lys Met Val Tyr  
180 185 190

Tyr Glu Glu Arg Ala Glu Met Tyr Val Gly Asp Asp Val Ser Pro Asp  
195 200 205

Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp His Val Ala Val Gly Thr

210	215	220
Gly Thr Val Thr His Lys Ala Asp Ile Lys Lys Phe Gln Ala Ala Thr		
225	230	235 240
Arg Leu Arg Ala Lys Asp Lys Ile Glu Gly Gly Lys Ile Ile Arg Val		
	245	250 255
Glu Ala His Pro Ile Pro Glu His Pro Arg Pro Lys Arg Val Ser Gly		
	260	265 270
Arg Val Thr Leu Val Gly Asp Ala Ala Gly Tyr Val Thr Lys Cys Ser		
	275	280 285
Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser Gly Arg Met Cys Ala Glu		
	290	295 300
Ala Ile Val Ala Gly Ser Ala Asn Gly Thr Arg Met Val Glu Glu Ser		
305	310	315 320
Asp Leu Arg Lys Tyr Leu Ala Glu Phe Asp Arg Leu Tyr Trp Pro Thr		
	325	330 335
Tyr Lys Val Leu Asp Ile Leu Gln Lys Val Phe Tyr Arg Ser Asn Ala		
	340	345 350
Ala Arg Glu Ala Phe Val Glu Met Cys Ala Asp Asp Tyr Val Gln Lys		
	355	360 365
Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg Val Val Pro Gly Asn Pro		
	370	375 380
Leu Asp Asp Ile Lys Leu Ala Val Asn Thr Ile Gly Ser Leu Val Arg		
385	390	395 400
Ala Thr Ala Leu Arg Arg Glu Met Glu Lys Val Thr Leu Xaa Ala Ala		
	405	410 415
Ala Arg Asp Val Ile Ala Val Glu Met Val Ser Gln Leu Ile Gly Arg		
	420	425 430
Cys Ile Ser Arg Asp Leu Arg Leu Ile Gly Leu Ile Xaa Ala Asn Met		
	435	440 445
Arg Gly Gln Trp Ala Arg Arg Gly Arg Glu Thr Ser Cys Ala Ser Ala		
	450	455 460
Ala Ser Arg Ser Lys Val Leu Pro Val Cys Ile Asp Gly Ser Cys Asn		

465	470	475	480
Ile Xaa His Leu Val Met Leu Arg Ile Arg Ser Ser Ser Ser Thr Gly			
485	490	495	
Phe Xaa Arg Arg Gln Ala Ser Thr Ser Met Asn Val Xaa Tyr Leu Val			
500	505	510	
His Gln Asp Met Xaa Xaa Asn Xaa Asn Ser Pro Val Leu Val Gln Lys			
515	520	525	
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Gly Arg			
530	535	540	

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<211> 80

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: transit peptide

<400> 31

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Ala Gly Ala Gly Met Val Ala Pro Phe Thr Gly Leu Lys Ser Met Ala			
20	25	30	
Gly Phe Pro Phe Thr Gly Leu Lys Ser Met Ala Gly Phe Pro Thr Arg			
35	40	45	
Lys Thr Asn Asn Asp Ile Thr Ser Ile Ala Ser Asn Gly Gly Arg Val			
50	55	60	
Gln Cys Met Gln Val Trp Pro Pro Ile Gly Lys Lys Lys Phe Glu Thr			
65	70	75	80